

1 CACAGACAGGCTCTTAACTGTTTATATCACTCACTTGGGAAAGTGTCTCAAGCTGTTCTA  
61 CAAATCCATGCAAAGGCCGTTTAAAAATAGCAGCGAAGGTCCTGGACTCGGTCTCGTCCA  
121 GCACAGCCCCTTGGCTCTCTCTCTGGGCTCTGGCCGCCTGGCCCCGGGGACCCACACGA  
181 GGTTCATGGCGTGTCTTCGGGCAGGGGGCGGGGATCCCATAGACACCTCAGCTCCTTAAGA  
241 GTTCTCCGCCTGGGCCAGGACGAGCATGGGGGTCCCCACTGATGCCCCGAGACAGTGCCCC  
301 TGTGTGTGTGAGCCCTCGACCCACATAACAGAGAGGTGTCCTGATGCCCTCTGTCTCTCTC  
361 CAGGTGGATCTAGGATCCGGCTTCCAACATGTGGCAGCTCTGGGCCTCCCTCTGCTGCCT  
421 GCTGGTGTGGCCAATGCCCGGAGCAGGCCCTCTTTCCATCCCGTGTGGGATGAGCTGGT  
481 CAACTATGTCAACAAACGGAATACCACGTGGCAGGCCGGGCACAACCTTCTACAACGTGGA  
541 CATGAGCTACTTGAAGAGGCTATGTGGTACCTTCCTGGGTGGGCCCCAAGCCACCCCAGAG  
601 AGTTATGTTTACCGAGGACCTGAAGCTGCCTGCAAGCTTCGATGCACGGGAACAATGGCC  
661 ACAGTGTCCCACCATCAAAGAGATCAGAGACCAGGGCTCCTGTGGCTCCTGCTGGGTAAG  
721 GCCCTGCTGGCTGGTGGGGAAGCGCTGGAGAGAAAGTGGGAGCAACACTGGAGAGTCTTG  
781 GGGGATTCGGGGTGGGGACAACCTCTGACAAGGCAAGTTATAGAACTTTCTGAGTCCCAG  
781 TTTCCATCAGTACAAAAATCACAATCCCTCTGGCCATGAATGATGGCGAGGATTAGGTGG  
841 AGTGGCGGGCAGAGCATCCAGCAGATTGCAAGTCCACGTGTACAGGTGGCGAAGCAGCTC  
901 CCTTTCCCTGACATGCTGGCCCGTCCGCAAATACCAGGAGCTCTCACTGCTACTCTGCTT  
961 CAAGAAAGCATCCCTTTAGTGTGTCAGTGAGCTGTCTTAATTTTGTCAATTAATTGTGGTAA  
1021 AATACACGTAACAGAAATGTAATAATCTTAGCAATCTTCTTTTGTTTTCTTTTTCTTTTT  
1081 TTTTTTTTTTTTTTTT

FIGURE 1

1 MWQLWASLCCLLVLANARSRPSFHPVSEDELVNYVKNRNTTWQAGHNFYNVDMSYKRLCG  
61 TFLGGPKPPQRMFTEDLKLPASFDAREQWPQCPTIKEIRDQSCGSCWVRPCWLVGKRW  
121 RESGSNTGESWGIRGGDNSDKASYRNFLSPSFHQYKNHNPSGHE

## FIGURE 2

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T06050" T6429460

1 TCCAAGTCCTGGATGAGCTCGGAAGACACGTGCTGCTGCGGAAGGACTGTGGCCCAGTGG  
61 ACACCAAGGTTCCAGGTGCTGGGGAGCCCAAGTCAGCCTTCACTCAGGGCTCAGCCATGA  
121 TTTCTTCTCTGTCCCAAACCATCCAGACAACAGAAACGAGACTTTTCAGCTCAGTCATTT  
181 CCCTGTTGAATGAGGATCCCCTGTCCCAGGACTTGCCTGTGAAGATGGCTTCAATCTTCA  
241 AGAACTTTGTCAATTACCTATAACCGGACATATGAGTCAAAGGAAGAAGCCCGGTGGCGCC  
301 TGTCCGTCTTTGTCAATAACATGGTGCGAGCACAGAAGATCCAGGCCCTGGACCGTGGCA  
361 CAGCTCAGTATGGAGTCACCAAGTTCAGTGATCTCACAGAGGAGGAGTTCGCACTATCT  
421 ACCTGAATACTCTCCTGAGGAAAGAGCCTGGCAACAAGATGAAGCAAGCCAAGTCTGTGG  
481 GTGACCTCGCCCCACCTGAATGGGACTGGAGGAGTAAGGGGGCTGTACAAAAGTCAAAG  
541 ACCAGGGCATGTGTGGCTCCTGCTGGGCCTTCTCAGTCACAGGCAATGTGGAGGGCCAGT  
601 GGTTCCTCAACCAGGGGACCCTGCTCTCCCTCTCTGAACAGGAGCTCTTGGACTGTGACA  
661 AGATGGACAAGGCCTGCATGGGCGGCTTGCCCTCCAATGCCTACTCGGCCATAAAGAATT  
721 TGGGAGGGCTGGAGACAGAGGATGACTACAGCTACCAGGGTCACATGCAGTCCTGCAACT  
781 TCTCAGCAGAGAAGGCCAAGGTCTACATCAATGACTCCGTGGAGCTGAGCCAGAACGAGC  
841 AGAAGCTGGCAGCCTGGCTGGCCAAGAGAGGCCCAATCTCCGTGGCCATCAATGCCTTTG  
901 GCATGCAGTTTTTACCGCCACGGGATCTCCCGCCCTCTCCGGCCCCTCTGCAGCCCTTGGC  
961 TCATTGACCATGCGGTGTTGCTTGTGGGCTACGGCAACCGCTCTGACGTTCCCTTTTGGG  
1021 CCATCAAGAACAGCTGGGGCACTGACTGGGGTGAGAAGGGTTACTACTACTTGCATCGCG  
1081 GGTCCGGGGCCTGTGGCGTGAACACCATGGCCAGCTCGGCGGTGGTGGACTGAAGAGGGG  
1141 CCCCCAGCTCGGGACCTGGTGCTGATCAGAGTGGCTGCTGCCCCAGCCTGACATGTGTCC  
1201 AGGCCCCTCCCCGGGAGGTACAGCTGGCAGAGGGAAAGGCACTGGGTACCTCAGGGTGAG  
1261 CAGAGGGCACTGGGCTGGGGCACAGCCCCTGCTT

FIGURE 3

1 MISSLSQNHDPNRFSSVISLLNEDPLSQDLPVKMASIFKNFVITYNRTYESKEEARW  
61 RLSVFVNNMVRAQKIQALDRGTAQYGVTKFSDLTEEEFRTIYLNTLLRKEPGNKMKAQS  
121 VGD LAPPEWDWR SKGAVTKVKDQGMCGSCWAFSVTGNVEGQWFLNQGTLLSLSEQELLDC  
181 DKMDKACMGGLPSNAYSIAKNLGGLETTEDDYSYQGHMQSCNFSAEKAKVYINDSVELSON  
241 EQKLA AWLAKRGPI SVAINAFGMQFYRHGISRPLRPLCSPWLIDHAVLLVG YGNRSDVPF  
301 WAIKNSWGTDWGEKGYYYLHRGSGACGVNTMASSAVVD

**FIGURE 4**

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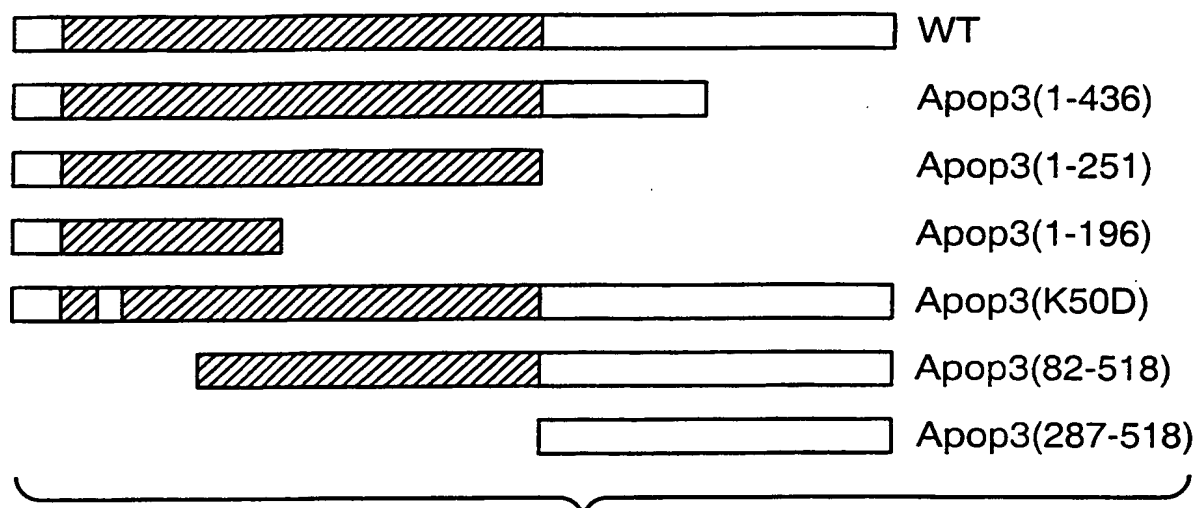
1 atgtcgtgcg tcaagttatg gccagcggt gccccgccc ccttggtgtc catcgaggaa  
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121 aggaagtggg gctacgatgt ggcggtcaag atcgtaaact cgaaggcgat atccagggag  
181 gtcaaggcca tggcaagtct ggataacgaa ttcgtgttgc gcctagaagg ggttatcgag  
241 aaggtgaact gggaccaaga tcccaagccg gctctggtga ctaaattcat ggagaacggc  
301 tccttgctcg ggctgctgca gtcccagtg cctcggccct ggccgctcct ttgccgctg  
361 ctgaaagaag tgggtgcttg gatgttttac ctgcacgacc agaacccggt gtcctgcac  
421 cgggacctca agccatccaa cgtcctgccg gacccagagc tgcacgtcaa gctggcagat  
481 tttggcctgt ccacatttca gggaggctca cagtcaggga cagggtccgg ggagccaggg  
541 ggcaccctgg gctacttggc ccagaactg tttgttaacg taaaccggaa ggcctccaca  
601 gccagtgacg tctacagctt cgggatccta atgtgggcag tgcttgctgg aagagaagtt  
661 gagttgccaa ccgaaccatc actcgtgtac gaagcagtgt gcaacaggca gaaccggcct  
721 tcattggctg agctgcccc a gccgggctt gagactcccg gcttagaagg actgaaggag  
781 ctaatgcagc tctgctggag cagtgcgccc aaggacagac cctccttcca ggaatgccta  
841 ccaaaaactg atgaagtctt ccagatggtg gagaacaata tgaatgctgc tgtctccacg  
901 gttaaaggatt tcctgtctca gctcaagagc agcaatagga gatttttctat cccagagtca  
961 ggccaaggag ggacagaaat ggatggcttt aggagaacca tagaaaacca gcactctcgt  
1021 aatgatgtca tgggtttctga gtggctaaac aaactgaatc tagaggagcc tcccagctct  
1081 gttcctaaaa aatgcccag cttaccaag aggagcaggg cacaagagga gcaggttcca  
1141 caagcctgga cagcaggcac atcttcagat tcgatggccc aacctcccca gactccagag  
1201 acctcaactt tcagaaacca gatgcccagc cctacctcaa ctggaacacc aagtccctgga  
1261 ccccagaggga atcagggggc tgagagacaa ggcatgaact ggtcctgcag gaccccgag  
1321 ccaaatccag taacaggggc accgctcgtt aacatataca actgctctgg ggtgcaagtt  
1381 ggagacaaca actacttgac tatgcaacag acaactgcct tgcccacatg gggcttggca  
1441 ccttcgggca aggggagggg cttgcagcac cccccaccag taggttcgca agaaggccct  
1501 aaagatcctg aagcctggag caggccacag ggttggtata atcatagcgg gaaataa

FIGURE 5

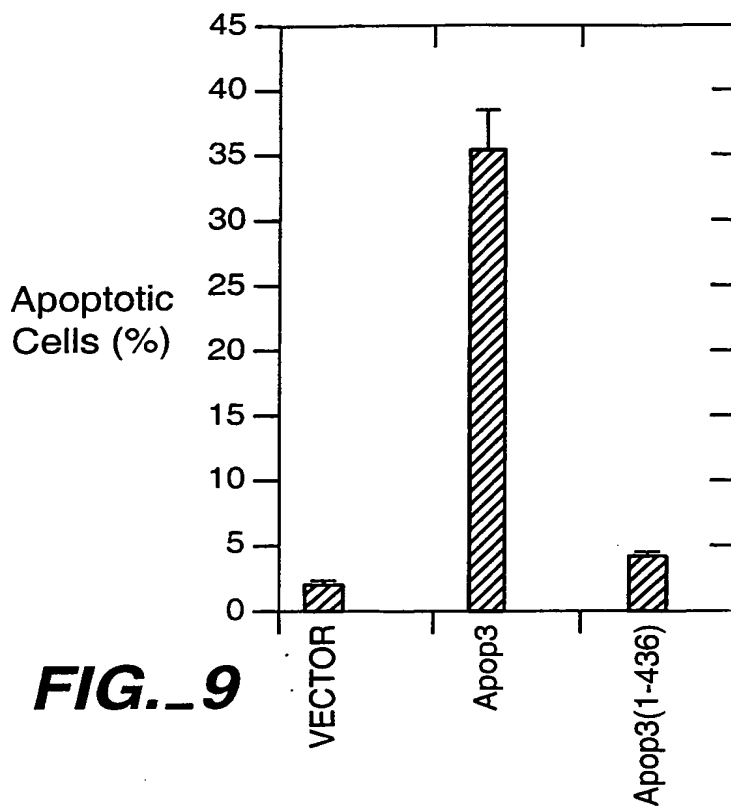
1 MSCVKLWPSGAPAPLVSIEELENQELVGKDGFGTVFRAQHRKWGYDVAVKIVNSKAISRE  
61 VKAMASLDNEFVLRLEGVIEKVNWDQDPKPALVTKFMENGSLSGLLQSQCPRPWPLLCLRL  
121 LKEVVLGMFYLDQNPVLLHRDLKPSNVLPDPELVKLAADFGLSTFQGGSQSGTGSGEPG  
181 GTLGYLAPELFVNVNRKASTASDVYSFGILMWAVLAGREVELPTEPSLVYEAVCNRQNRP  
241 SLAELPQAGPETPGLEGLKELMQLCWSSEP KDRPSFQECLPKTDEVFQMVENNMNAAVST  
301 VKDFLSQLKSSNRRFSIPESGQGGTEMDGFRRTIENQHSRNDVMVSEWLNKLNLEPPSS  
361 VPKKCPSLTKRSRAQEEQVPQAWTAGTSSDSMAQPPQTPETSTFRNQMPSPSTSTGTPSPG  
421 PRGNQGAERQGMNWSCRTPEPNPVTGRPLVNIYNCSGVQVGDNNYLTMQQTALPTWGLA  
481 PSGKGRGLQHPPPVGSQEGPKDPEAWSRPQGWYNHSGKZ

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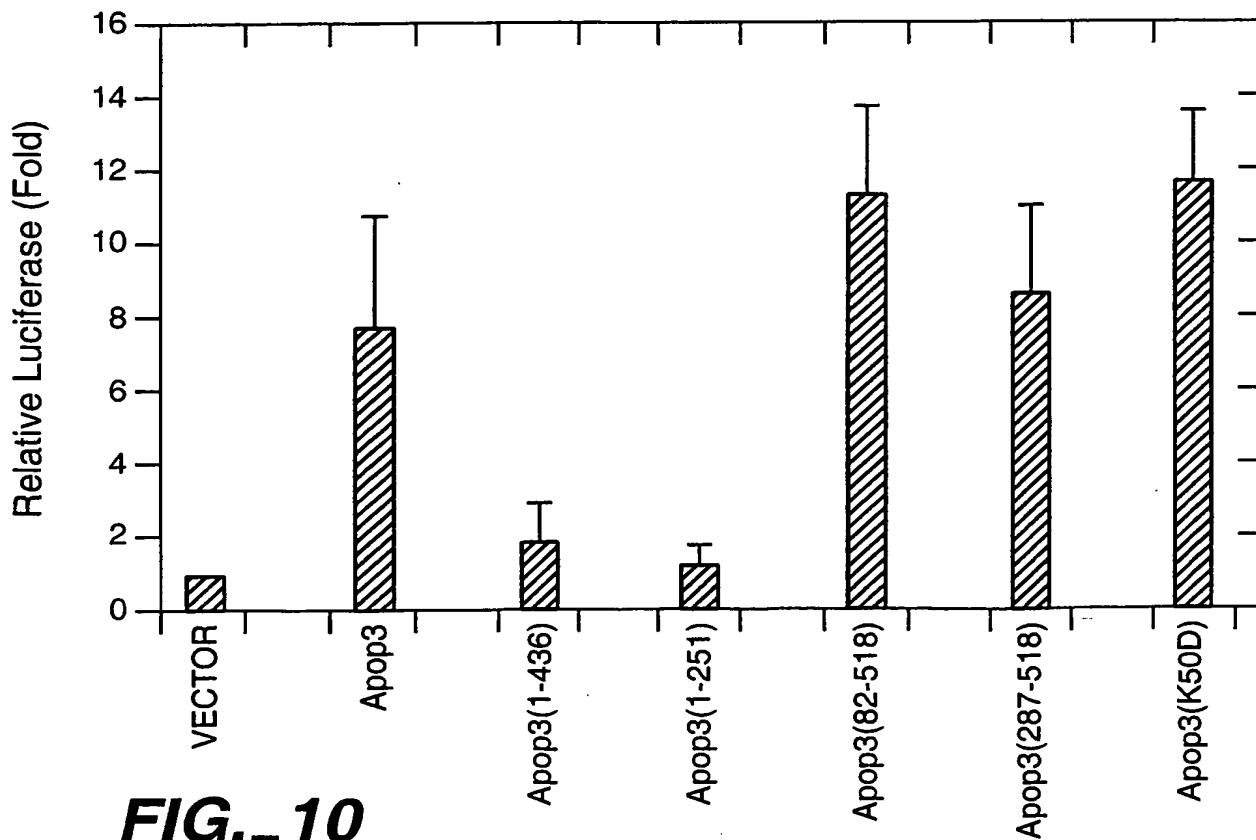
## FIGURE 6

**FIG.\_7**

		Binding To RIP
<b>FIG._8</b>	Apop3	++++
	Apop3(1-436)	+
	Apop3(1-251)	-
	Apop3(1-196)	-
	Apop3(K50D)	++++
	Apop3(82-518)	+++
	Apop3(287-518)	-



**FIG. 9**



**FIG. 10**